



SEQUENCE LISTING

<110> Barry, Gerard F.
Kishore, Ganesh M.
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Stallings, William C.

<120> GLYPHOSATE TOLERANT 5-ENOLPYRUVYL SHIKIMATE-3-PHOSPHATE SYNTHASES

<130> 11899.0175.REUS07

<140> 10/622,201
<141> 2003-07-18

<150> US 08/306,063
<151> 1994-09-13

<150> US 07/749,611
<151> 1991-08-28

<150> US 07/576,537
<151> 1990-08-31

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cggtcc ttc atg ttc ggc ggt ctc gcg agc ggt gaa acg cgc atc acc 205
 Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
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gcc atg ggc gcc agg atc cgt aag gaa ggc gac acc tgg atc atc gat 301
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 Gly Val Gly Asn Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
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Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser	
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Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu	
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Leu Ser Asp Thr Lys Ala Ala	
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Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
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Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
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Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
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Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
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Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
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His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
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Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
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ggc gac aag tcc atc tcg cat cgc tcc ttc atg ttt ggc ggt ctc gca 208
Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala
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Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile
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Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu
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Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln
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Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu
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cgc gaa atg ggc gtt cag gtg gaa gca gcc gat ggc gac cgc atg ccg Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro 140 145 150	544
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Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly			
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Ala Lys Ile Glu Leu Ser Ile Leu			
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Val Ile Glu Pro Val Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
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Gly Phe Gly Ala Asp Leu Thr Val Glu Thr Asp Lys Asp Gly Val Arg
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His Ile Arg Ile Thr Gly Gln Gly Lys Leu Val Gly Gln Thr Ile Asp
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His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Ala Ala Glu Lys
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Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg
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Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly
25 30 35

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Leu Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp
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Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg
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Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu
75 80 85

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Arg Leu Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe	
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Ile Gly Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn	
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Val Glu Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln	
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Gly Lys Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser	
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Tyr Pro Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val	
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Ala Val Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly	
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Glu Met Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly	
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Gly Gly Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe	
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ctc gtg atg ggc ctt gcg gcg gaa aag ccg gtg acg gtt gac gac agt	1302
Leu Val Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser	
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440 445	
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cttccatacgt taacagcatc aggaaatatc aaaaaagctt	1500
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<213> Pseudomonas sp.	
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Ala Leu Thr Gly Glu Ile Arg Ile Pro Gly Asp Lys Ser Ile Ser His	
20 25 30	
Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr	
35 40 45	

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Arg Ala Met Gln
 50 55 60

Ala Met Gly Ala Lys Ile Arg Lys Glu Gly Asp Val Trp Ile Ile Asn
 65 70 75 80

Gly Val Gly Asn Gly Cys Leu Leu Gln Pro Glu Ala Ala Leu Asp Phe
 85 90 95

Gly Asn Ala Gly Thr Gly Ala Arg Leu Thr Met Gly Leu Val Gly Thr
 100 105 110

Tyr Asp Met Lys Thr Ser Phe Ile Gly Asp Ala Ser Leu Ser Lys Arg
 115 120 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
 130 135 140

Glu Ala Ala Asp Gly Asp Arg Met Pro Leu Thr Leu Ile Gly Pro Lys
 145 150 155 160

Thr Ala Asn Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
 165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Val Thr Thr
 180 185 190

Val Ile Glu Pro Val Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
 195 200 205

Gly Phe Gly Ala Asp Leu Thr Val Glu Thr Asp Lys Asp Gly Val Arg
 210 215 220

His Ile Arg Ile Thr Gly Gln Gly Lys Leu Val Gly Gln Thr Ile Asp
 225 230 235 240

Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
 245 250 255

Leu Val Glu Gly Ser Asp Val Thr Ile Arg Asn Val Leu Met Asn Pro
 260 265 270

Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
 275 280 285

Glu Val Leu Asn Ala Arg Leu Ala Gly Glu Asp Val Ala Asp Leu
 290 295 300

Arg Val Arg Ala Ser Lys Leu Lys Gly Val Val Val Pro Pro Glu Arg
 305 310 315 320

Ala Pro Ser Met Ile Asp Glu Tyr Pro Val Leu Ala Ile Ala Ala Ser
 325 330 335

Phe Ala Glu Gly Glu Thr Val Met Asp Gly Leu Asp Glu Leu Arg Val
 340 345 350

Lys	Glu	Ser	Asp	Arg	Leu	Ala	Ala	Val	Ala	Arg	Gly	Leu	Glu	Ala	Asn
355					360							365			
Gly	Val	Asp	Cys	Thr	Glu	Gly	Glu	Met	Ser	Leu	Thr	Val	Arg	Gly	Arg
370					375							380			
Pro	Asp	Gly	Lys	Gly	Leu	Gly	Gly	Thr	Val	Ala	Thr	His	Leu	Asp	
385					390							395			400
His	Arg	Ile	Ala	Met	Ser	Phe	Leu	Val	Met	Gly	Leu	Ala	Ala	Glu	Lys
					405						410			415	
Pro	Val	Thr	Val	Asp	Asp	Ser	Asn	Met	Ile	Ala	Thr	Ser	Phe	Pro	Glu
					420						425			430	
Phe	Met	Asp	Met	Met	Pro	Gly	Leu	Gly	Ala	Lys	Ile	Glu	Leu	Ser	Ile
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Leu

<210>	8
<211>	423
<212>	PRT
<213>	Escherichia coli

<400>	8
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Ser	Leu	Thr	Leu	Gln	Pro	Ile	Ala	Arg	Val	Asp	Gly	Thr	Ile	Asn	Leu
1				5				10					15		

Pro	Gly	Ser	Lys	Thr	Val	Ser	Asn	Arg	Ala	Leu	Leu	Leu	Ala	Ala	Leu
					20								30		

Ala	His	Gly	Lys	Thr	Val	Leu	Thr	Asn	Leu	Leu	Asp	Ser	Asp	Asp	Val
													35	40	45

Arg	His	Met	Leu	Asn	Ala	Leu	Thr	Ala	Leu	Gly	Val	Ser	Tyr	Thr	Leu
													50	55	60

Ser	Ala	Asp	Arg	Thr	Arg	Cys	Glu	Ile	Ile	Gly	Asn	Gly	Gly	Pro	Leu	
													65	70	75	80

His	Ala	Glu	Gly	Ala	Leu	Glu	Leu	Phe	Leu	Gly	Asn	Ala	Gly	Thr	Ala	
													85	90	95	

Met	Arg	Pro	Leu	Ala	Ala	Leu	Cys	Leu	Gly	Ser	Asn	Asp	Ile	Val		
													100	105	110	

Leu	Thr	Gly	Glu	Pro	Arg	Met	Lys	Glu	Arg	Pro	Ile	Gly	His	Leu	Val	
													115	120	125	

Asp	Ala	Leu	Arg	Leu	Gly	Gly	Ala	Lys	Ile	Thr	Tyr	Leu	Glu	Gln	Glu	
													130	135	140	

Asn	Tyr	Pro	Pro	Leu	Arg	Leu	Gln	Gly	Gly	Phe	Thr	Gly	Gly	Asn	Val	
													145	150	155	160


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<210> 9
<211> 1377
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

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tcgctagcgg tgaaactcgt atcaccggtc ttttggagg tgaagatgtt atcaacactg      180
gtaaggctat gcaagctatg ggtgccagaa tccgtaagga aggtgatact tggatcattg      240
atggtgttgg taacggtgga ctcccttgctc ctgaggctcc tctcgatttc ggtaacgctg      300
caactggttg ccgtttgact atgggtcttg ttgggttta cgatttcgat agcacttca      360
ttggtgacgc ttctctcaact aagcgtccaa tgggtcgtgt gttgaaccca cttcgcgaaa      420
tgggtgtgca ggtgaagtct gaagacggtg atcgcttcc agttaccttgcgtggaccaa      480
agactccaac gccaatcacc tacagggta ctagggcttc cgctcaagtg aagtccgctg      540
ttctgcttgc tggtctcaac accccaggtt tcaccactgt tatcgagcca atcatgactc      600
gtgaccacac tggaaagatg cttcaagggtt ttggtgctaa ctttaccgtt gagactgatg      660
ctgacggtgtt gcgtaccatc cgtcttgaag gtcgtggtaa gtcaccggtaa caagtgattt      720
atgttccagg tgatccatcc tctactgctt tcccattgggt tgctgccttgcgttccagg      780
gttccgacgt caccatcctt aacgttttga tgaacccaac ccgtactggtaa ctcatcttgc      840
ctctgcagga aatgggtgcc gacatcgaag tgatcaaccc acgtcttgcgtt ggtggagaag      900
acgtggctga cttgcgtgtt cgttcttcta ctttgaaggg tgttactgtt ccagaagacc      960
gtgctcccttc tatgatcgac gagtatccaa ttctcgctgt tgctgcgtca ttgcgtgaag      1020
gtgctaccgt tatgaacggt ttggagaac tccgtgtttaa ggaaagcgac cgtcttctg      1080
ctgtcgcaaa cggctcaag cttcaacggtg ttgattgcga tgaagggtgag acttctctcg      1140
tcgtgcgtgg tcgtccctgac ggttgggtc tcggtaacgc ttctggagca gctgtcgcta      1200
cccacctcga tcaccgtatc gctatgagct tccctcggtt gggctcggt tctgaaaacc      1260
ctgttactgt tgatgatgct actatgatcg ctactagctt cccagagttc atggatttga      1320
tggctggtct tggagactaag atcgaactct ccgacactaa ggctgcttga tgagctc      1377

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<210> 10
<211> 318
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (87)..(317)

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cgattgcttc aattgaagtt tctccg atg gcg caa gtt agc aga atc tgc aat      113
          Met Ala Gln Val Ser Arg Ile Cys Asn
          1           5

ggt gtg cag aac cca tct ctt atc tcc aat ctc tcg aaa tcc agt caa      161
Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln
10          15           20           25

cgc aaa tct ccc tta tcg gtt tct ctg aag acg cag cag cat cca cga      209
Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln Gln His Pro Arg
30          35           40

gct tat ccg att tcg tcg tgg gga ttg aag aag agt ggg atg acg      257
Ala Tyr Pro Ile Ser Ser Trp Gly Leu Lys Ser Gly Met Thr
45          50           55

tta att ggc tct gag ctt cgt cct ctt aag gtc atg tct tct gtt tcc      305
Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Ser Val Ser
60          65           70

acg gcg tgc atg c      318
Thr Ala Cys Met
75

<210> 11
<211> 77
<212> PRT
<213> Arabidopsis thaliana

<400> 11

Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu
1          5           10           15

Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val
20         25           30

Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser
35         40           45

Trp Gly Leu Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg
50         55           60

Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Cys Met
65         70           75

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<210> 12
 <211> 402
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (87)..(401)

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 Met Ala Gln Val Ser Arg Ile Cys Asn
 1 5

ggt gtg cag aac cca tct ctt atc tcc aat ctc tcg aaa tcc agt caa 161
 Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln
 10 15 20 25

cgc aaa tct ccc tta tcg gtt tct ctg aag acg cag cag cat cca cga 209
 Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln Gln His Pro Arg
 30 35 40

gct tat ccg att tcg tcg tgg gga ttg aag aag agt ggg atg acg 257
 Ala Tyr Pro Ile Ser Ser Trp Gly Leu Lys Ser Gly Met Thr
 45 50 55

tta att ggc tct gag ctt cgt cct ctt aag gtc atg tct tct gtt tcc 305
 Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Ser Val Ser
 60 65 70

acg gcg gag aaa gcg tcg gag att gta ctt caa ccc att aga gaa atc 353
 Thr Ala Glu Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile
 75 80 85

tcc ggt ctt att aag ttg cct ggc tcc aag tct cta tca aat aga att c 402
 Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile
 90 95 100 105

<210> 13
 <211> 105
 <212> PRT
 <213> Arabidopsis thaliana

<400> 13
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 Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val 20 25 30
 Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser 35 40 45

Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg
50 55 60

Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Glu Lys Ala Ser Glu
65 70 75 80

Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu Ile Lys Leu Pro
85 90 95

Gly Ser Lys Ser Leu Ser Asn Arg Ile
100 105

<210> 14

<211> 233

<212> DNA

<213> Petunia x hybrida

<220>

<221> CDS

<222> (14) .. (232)

<400> 14

agatctttca aga atg gca caa att aac aac atg gct caa ggg ata caa 49
Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln
1 5 10

acc ctt aat ccc aat tcc aat ttc cat aaa ccc caa gtt cct aaa tct 97
Thr Leu Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser
15 20 25

tca agt ttt ctt gtt ttt gga tct aaa aaa ctg aaa aat tca gca aat 145
Ser Ser Phe Leu Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn
30 35 40

tct atg ttg gtt ttg aaa aaa gat tca att ttt atg caa aag ttt tgt 193
Ser Met Leu Val Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys
45 50 55 60

tcc ttt agg att tca gca tca gtg gct aca gcc tgc atg c 233
Ser Phe Arg Ile Ser Ala Ser Val Ala Thr Ala Cys Met
65 70

<210> 15

<211> 73

<212> PRT

<213> Petunia x hybrida

<400> 15

Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro
1 5 10 15

Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu
20 25 30

Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val
35 40 45

Leu	Lys	Lys	Asp	Ser	Ile	Phe	Met	Gln	Lys	Phe	Cys	Ser	Phe	Arg	Ile
50															60
Ser Ala Ser Val Ala Thr Ala Cys Met															
65															70
<210> 16															
<211> 352															
<212> DNA															
<213> Petunia x hybrida															
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<221> CDS															
<222> (49)..(351)															
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agatctgcta gaaataattt tggttaactt taagaaggag atatatcc atg gca caa															
Met Ala Gln															
1															
att aac aac atg gct caa ggg ata caa acc ctt aat ccc aat tcc aat															
Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro Asn Ser Asn															
5	10	15													105
ttc cat aaa ccc caa gtt cct aaa tct tca agt ttt ctt gtt ttt gga															
Phe His Lys Pro Gln Val Pro Lys Ser Ser Phe Leu Val Phe Gly															
20	25	30	35												153
tct aaa aaa ctg aaa aat tca gca aat tct atg ttg gtt ttg aaa aaa															
Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val Leu Lys Lys															
40	45	50													201
gat tca att ttt atg caa aag ttt tgt tcc ttt agg att tca gca tca															
Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile Ser Ala Ser															
55	60	65													249
gtg gct aca gca cag aag cct tct gag ata gtg ttg caa ccc att aaa															
Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys															
70	75	80													297
gag att tca ggc act gtt aaa ttg cct ggc tct aaa tca tta tct aat															
Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn															
85	90	95													345
aga att c															
Arg Ile															
100															352

<210> 17
<211> 101
<212> PRT
<213> Petunia x hybrida

<400> 17

Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro
1 5 10 15

Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu
20 25 30

Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val
35 40 45

Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile
50 55 60

Ser Ala Ser Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln
65 70 75 80

Pro Ile Lys Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser
85 90 95

Leu Ser Asn Arg Ile
100

<210> 18
<211> 28
<212> PRT
<213> Agrobacterium sp.

<220>
<221> UNSURE
<222> (1)...(18)
<223> Xaa = Unknown

<400> 18

Xaa His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser Gly
1 5 10 15

Leu Xaa Gly Thr Val Arg Ile Pro Gly Asp Lys Met
20 25

<210> 19
<211> 13
<212> PRT
<213> Agrobacterium sp.

<400> 19

Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val
1 5 10

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<210> 20
<211> 15
<212> PRT
<213> Agrobacterium sp.

<400> 20

Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys
1           5           10           15

<210> 21
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 21
atgathgayg artaycc                                17

<210> 22
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (1)..(17)
<223> R = A or G;

Y = C or T/U;

N = A or C or G or T/U;

H = A or C or T/U

<400> 22
gargaygtna thaacac                                17

<210> 23
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (1)..(17)
<223> R = A or G;
Y = C or T/U;

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N = A or C or G or T/U;
H = A or C or T/U

<400> 23	
gargaygtna thaatac	17
<210> 24	
<211> 38	
<212> DNA	
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<400> 24	
cgtggataga tctaggaaga caaccatggc tcacggtc	38
<210> 25	
<211> 44	
<212> DNA	
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<210> 26	
<211> 35	
<212> DNA	
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<220>	
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<400> 26	
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<210> 27	
<211> 32	
<212> DNA	
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<220>	
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<400> 27	
cgtcgctcgt cgtgcgtggc cggccctgacg gc	32
<210> 28	
<211> 29	
<212> DNA	
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<220>	
<223> Oligonucleotide	

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<400> 28
cgggcaaggc catgcaggct atgggcgcc 29

<210> 29
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 29
cgggctgccg cctgactatg gcgcctcg 31
cgt g

<210> 30
<211> 15
<212> PRT
<213> Pseudomonas sp.

<220>
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<222> (1)..(1)
<223> Xaa = unknown

<400> 30

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1 5 10 15

<210> 31
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<220>
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<222> (1)..(17)
<223> B = C or G or T

S = G or C

Y = C or T

<400> 31
gcgtbgsy gyttsgg 17

<210> 32
<211> 16
<212> PRT
<213> Artificial sequence

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<220>
<223> Synthetic
<400> 32

Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu
1 5 10 15

<210> 33
<211> 13
<212> PRT
<213> Artificial sequence

<220>
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<400> 33

Leu Asp Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr
1 5 10

<210> 34
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 34
cgccaatgcc gccaccggcg cgcgcc

26

<210> 35
<211> 49
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 35
ggacggctgc ttgcaccgtg aagcatgctt aagcttggcg taatcatgg

49

<210> 36
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 36
ggaagacgccc cagaattcac ggtgcaagca gccgg

35

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<210> 37
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> NON_CONS
<222> (2)..(2)
<223> Xaa = Gly, Ser, Thr, Cys, Tyr, Asn, Gln, Asp, or Glu

<220>
<221> NON_CONS
<222> (4)..(4)
<223> Xaa = Ser or Thr

<400> 37

Arg Xaa His Xaa Glu
1 5

<210> 38
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> NON_CONS
<222> (4)..(4)
<223> Xaa = Ser or Thr

<400> 38

Gly Asp Lys Xaa
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<210> 39
<211> 5
<212> PRT
<213> Artificial sequence

<220>
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<220>
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<222> (4)..(4)
<223> Xaa=Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys,
      Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val

<400> 39

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Ser Ala Gln Xaa Lys
 1 5

<210> 40
 <211> 4
 <212> PRT
 <213> Artificial sequence

<220>
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<220>
 <221> NON_CONS
 <222> (2)..(2)
 <223> Xaa=Ala, Arg, Asn, Asp, Cys, Iu, Iu, Iy, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val

<400> 40

Asn Xaa Thr Arg
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<210> 41
 <211> 1287
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1287)

<400> 41

atg	aaa	cga	gat	aag	gtg	cag	acc	tta	cat	gga	gaa	ata	cat	att	ccc	48
Met	Lys	Arg	Asp	Lys	Val	Gln	Thr	Leu	His	Gly	Glu	Ile	His	Ile	Pro	
1		5				10							15			

ggt	aat	tcc	att	tct	cac	cgc	tct	gtt	atg	ttt	ggc	gct	cta	gct	96	
Gly	Asp	Lys	Ser	Ile	Ser	His	Arg	Ser	Val	Met	Phe	Gly	Ala	Leu	Ala	
20					25							30				

gca	ggc	aca	aca	aca	gtt	aaa	aac	ttt	ctg	ccg	gga	gca	gat	tgt	ctg	144
Ala	Gly	Thr	Thr	Val	Lys	Asn	Phe	Leu	Pro	Gly	Ala	Asp	Cys	Leu		
35					40							45				

agc	acg	atc	gat	tgc	ttt	aga	aaa	atg	ggt	cac	att	gag	caa	agc	192	
Ser	Thr	Ile	Asp	Cys	Phe	Arg	Lys	Met	Gly	Val	His	Ile	Glu	Gln	Ser	
50					55						60					

agc	agc	gat	gtc	gtg	att	cac	gga	aaa	gga	atc	gat	gcc	ctg	aaa	gag	240
Ser	Ser	Asp	Val	Val	Ile	His	Gly	Lys	Gly	Ile	Asp	Ala	Leu	Lys	Glu	
65					70				75				80			

cca	gaa	agc	ctt	tta	gat	gtc	gga	aat	tca	ggt	aca	acg	att	cgc	ctg	288
Pro	Glu	Ser	Leu	Leu	Asp	Val	Gly	Asn	Ser	Gly	Thr	Thr	Ile	Arg	Leu	
85					90							95				

atg ctc gga ata ttg gcg ggc cgt cct ttt tac agc gcg gta gcc gga Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly 100 105 110	336
gat gag agc att gcg aaa cgc cca atg aag cgt gtg act gag cct ttg Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu 115 120 125	384
aaa aaa atg ggg gct aaa atc gac ggc aga gcc ggc gga gag ttt aca Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr 130 135 140	432
ccg ctg tca gtg agc ggc gct tca tta aaa gga att gat tat gta tca Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser 145 150 155 160	480
cct gtt gca agc gcg caa att aaa tct gct gtt ttg ctg gcc gga tta Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu 165 170 175	528
cag gct gag ggc aca aca act gta aca gag ccc cat aaa tct cgg gac Gln Ala Glu Gly Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp 180 185 190	576
cac act gag cgg atg ctt tct gct ttt ggc gtt aag ctt tct gaa gat His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp 195 200 205	624
caa acg agt gtt tcc att gct ggt ggc cag aaa ctg aca gct gct gat Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp 210 215 220	672
att ttt gtt cct gga gac att tct tca gcc gcg ttt ttc ctt gct gct Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala 225 230 235 240	720
ggc gcg atg gtt cca aac agc aga att gta ttg aaa aac gta ggt tta Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu 245 250 255	768
aat ccg act cgg aca ggt att att gat gtc ctt caa aac atg ggg gca Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala 260 265 270	816
aaa ctt gaa atc aaa cca tct gct gat agc ggt gca gag cct tat gga Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly 275 280 285	864
gat ttg att ata gaa acg tca tct cta aag gca gtt gaa atc gga gga Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly 290 295 300	912
gat atc att ccg cgt tta att gat gag atc cct atc atc gcg ctt ctt Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu 305 310 315 320	960

gcg act cag gcg gaa gga acc acc gtt att aag gac gcg gca gag cta	1008
Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu	
325 330 335	
aaa gtg aaa gaa aca aac cgt att gat act gtt gtt tct gag ctt cgc	1056
Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Val Ser Glu Leu Arg	
340 345 350	
aag ctg ggt gct gaa att gaa ccg aca gca gat gga atg aag gtt tat	1104
Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr	
355 360 365	
ggc aaa caa acg ttg aaa ggc ggc gct gca gtg tcc agc cac gga gat	1152
Gly Lys Gln Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp	
370 375 380	
cat cga atc gga atg atg ctt ggt att gct tcc tgt ata acg gag gag	1200
His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu	
385 390 395 400	
ccg att gaa atc gag cac acg gat gcc att cac gtt tct tat cca acc	1248
Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr	
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Phe Phe Glu His Leu Asn Lys Leu Ser Lys Lys Ser	
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35 40 45	
Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser	
50 55 60	
Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu	
65 70 75 80	
Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu	
85 90 95	
Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly	
100 105 110	

Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu
 115 120 125
 Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr
 130 135 140
 Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser
 145 150 155 160
 Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu
 165 170 175
 Gln Ala Glu Gly Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp
 180 185 190
 His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp
 195 200 205
 Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp
 210 215 220
 Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala
 225 230 235 240
 Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu
 245 250 255
 Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala
 260 265 270
 Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly
 275 280 285
 Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly
 290 295 300
 Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu
 305 310 315 320
 Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu
 325 330 335
 Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Val Ser Glu Leu Arg
 340 345 350
 Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr
 355 360 365
 Gly Lys Gln Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp
 370 375 380
 His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu
 385 390 395 400
 Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr
 405 410 415

Phe	Phe	Glu	His	Leu	Asn	Lys	Leu	Ser	Lys	Lys	Ser					
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Met	Val	Asn	Glu	Gln	Ile	Ile	Asp	Ile	Ser	Gly	Pro	Leu	Lys	Gly	Glu	
1									10					15		
ata	gaa	gtg	ccg	ggc	gat	aag	tca	atg	aca	cac	cgt	gca	atc	atg	ttg	96
Ile	Glu	Val	Pro	Gly	Asp	Lys	Ser	Met	Thr	His	Arg	Ala	Ile	Met	Leu	
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gcg	tcg	cta	gct	gaa	ggt	gta	tct	act	ata	tat	aag	cca	cta	ctt	ggc	144
Ala	Ser	Leu	Ala	Glu	Gly	Val	Ser	Thr	Ile	Tyr	Lys	Pro	Leu	Leu	Gly	
35									40					45		
gaa	gat	tgt	cgt	acg	atg	gac	att	ttc	cga	cac	tta	ggt	gta	gaa	192	
Glu	Asp	Cys	Arg	Arg	Thr	Met	Asp	Ile	Phe	Arg	His	Leu	Gly	Val	Glu	
50									55					60		
atc	aaa	gaa	gat	gat	gaa	aaa	tta	gtt	gtg	act	tcc	cca	gga	tat	caa	240
Ile	Lys	Glu	Asp	Asp	Glu	Lys	Leu	Val	Val	Thr	Ser	Pro	Gly	Tyr	Gln	
65									70					75		
gtt	aac	acg	cca	cat	caa	gta	ttg	tat	aca	ggt	aat	tct	ggt	acg	aca	288
Val	Asn	Thr	Pro	His	Gln	Val	Tyr	Thr	Gly	Asn	Ser	Gly	Thr	Thr		
85									90					95		
aca	cga	tta	ttg	gca	ggt	ttg	tta	agt	ggt	aat	gaa	agt	gtt			336
Thr	Arg	Leu	Leu	Ala	Gly	Leu	Leu	Ser	Gly	Leu	Gly	Asn	Glu	Ser	Val	
100									105					110		
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Leu	Ser	Gly	Asp	Val	Ser	Ile	Gly	Lys	Arg	Pro	Met	Asp	Arg	Val	Leu	
115									120					125		
aga	cca	ttg	aaa	ctt	atg	gat	gca	aat	att	gaa	ggt	att	gaa	gat	aat	432
Arg	Pro	Leu	Lys	Leu	Met	Asp	Ala	Asn	Ile	Glu	Gly	Ile	Glu	Asp	Asn	
130									135					140		
tat	aca	cca	tta	att	att	aag	cca	tct	gtc	ata	aaa	ggt	ata	aat	tat	480
Tyr	Thr	Pro	Leu	Ile	Ile	Lys	Pro	Ser	Val	Ile	Lys	Gly	Ile	Asn	Tyr	
145									150					155		
caa	atg	gaa	gtt	gca	agt	gca	caa	gta	aaa	agt	gcc	att	tta	ttt	gca	528
Gln	Met	Glu	Val	Ala	Ser	Ala	Gln	Val	Lys	Ser	Ala	Ile	Leu	Phe	Ala	
165									170					175		

agt ttg ttt tct aag gaa ccg acc atc att aaa gaa tta gat gta agt Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser 180 185 190	576
cga aat cat act gag acg atg ttc aaa cat ttt aat att cca att gaa Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu 195 200 205	624
gca gaa ggg tta tca att aat aca acc cct gaa gca att cga tac att Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile 210 215 220	672
aaa cct gca gat ttt cat gtt cct ggc gat att tca tct gca gcg ttc Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe 225 230 235 240	720
ttt att gtt gca gca ctt atc aca cca gga agt gat gta aca att cat Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His 245 250 255	768
aat gtt gga atc aat caa aca cgt tca ggt att att gat att gtt gaa Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu 260 265 270	816
aaa atg ggc ggt aat atc caa ctt ttc aat caa aca act ggt gct gaa Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Gly Ala Glu 275 280 285	864
cct act gct tct att cgt att caa tac aca cca atg ctt caa cca ata Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile 290 295 300	912
aca atc gaa gga gaa tta gtt cca aaa gca att gat gaa ctg cct gta Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val 305 310 315 320	960
ata gca tta ctt tgt aca caa gca gtt ggc acg agt aca att aaa gat Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp 325 330 335	1008
gcc gag gaa tta aaa gta aaa gaa aca aat aga att gat aca acg gct Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala 340 345 350	1056
gat atg tta aac ttg tta ggg ttt gaa tta caa cca act aat gat gga Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly 355 360 365	1104
ttg att att cat ccg tca gaa ttt aaa aca aat gca aca gat att tta Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu 370 375 380	1152
act gat cat cga ata gga atg atg ctt gca gtt gct tgt gta ctt tca Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser 385 390 395 400	1200

agc gag cct gtc aaa atc aaa caa ttt gat gct gta aat gta tca ttt	405	410	415	1248
Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe				
cca gga ttt tta cca aaa cta aag ctt tta caa aat gag gga taa	420	425	430	1293
Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly				
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Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu	20	25	30	
Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly	35	40	45	
Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu	50	55	60	
Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln	65	70	75	80
Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr	85	90	95	
Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val	100	105	110	
Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu	115	120	125	
Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn	130	135	140	
Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr	145	150	155	160
Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala	165	170	175	
Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser	180	185	190	
Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu	195	200	205	
Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile	210	215	220	

Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe
 225 230 235 240

 Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His
 245 250 255

 Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu
 260 265 270

 Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu
 275 280 285

 Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile
 290 295 300

 Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val
 305 310 315 320

 Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp
 325 330 335

 Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala
 340 345 350

 Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly
 355 360 365

 Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu
 370 375 380

 Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser
 385 390 395 400

 Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe
 405 410 415

 Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly
 420 425 430

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 <220>
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28

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Gln Gln Lys Val Val Ile Pro Pro Gly Ser Lys Ser Ile Ser Asn Arg	
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Ala Leu Ile Leu Ala Ala Leu Gly Glu Gly Gln Cys Lys Ile Lys Asn	
35 40 45	
Leu Leu His Ser Asp Asp Thr Lys His Met Leu Thr Ala Val His Glu	
50 55 60	
Leu Lys Gly Ala Thr Ile Ser Trp Glu Asp Asn Gly Glu Thr Val Val	
65 70 75 80	
Val Glu Gly His Gly Ser Thr Leu Ser Ala Cys Ala Asp Pro Leu	
85 90 95	
Tyr Leu Gly Asn Ala Gly Thr Ala Ser Arg Phe Leu Thr Ser Leu Ala	
100 105 110	
Ala Leu Val Asn Ser Thr Ser Ser Gln Lys Tyr Ile Val Leu Thr Gly	
115 120 125	

Asn Ala Arg Met Gln Gln Arg Pro Ile Ala Pro Leu Val Asp Ser Leu
 130 135 140
 Arg Ala Asn Gly Thr Lys Ile Glu Tyr Leu Asn Asn Glu Gly Ser Leu
 145 150 155 160
 Pro Ile Lys Val Tyr Thr Asp Ser Val Phe Lys Gly Gly Arg Ile Glu
 165 170 175
 Leu Ala Ala Thr Val Ser Ser Gln Tyr Val Ser Ser Ile Leu Met Cys
 180 185 190
 Ala Pro Tyr Ala Glu Glu Pro Val Thr Leu Ala Leu Val Gly Gly Lys
 195 200 205
 Pro Ile Ser Lys Leu Tyr Val Asp Met Thr Ile Lys Met Met Glu Lys
 210 215 220
 Phe Gly Ile Asn Val Glu Thr Ser Thr Thr Glu Pro Tyr Thr Tyr Tyr
 225 230 235 240
 Ile Pro Lys Gly His Tyr Ile Asn Pro Ser Glu Tyr Val Ile Glu Ser
 245 250 255
 Asp Ala Ser Ser Ala Thr Tyr Pro Leu Ala Phe Ala Ala Met Thr Gly
 260 265 270
 Thr Thr Val Thr Val Pro Asn Ile Gly Phe Glu Ser Leu Gln Gly Asp
 275 280 285
 Ala Arg Phe Ala Arg Asp Val Leu Lys Pro Met Gly Cys Lys Ile Thr
 290 295 300
 Gln Thr Ala Thr Ser Thr Thr Val Ser Gly Pro Pro Val Gly Thr Leu
 305 310 315 320
 Lys Pro Leu Lys His Val Asp Met Glu Pro Met Thr Asp Ala Phe Leu
 325 330 335
 Thr Ala Cys Val Val Ala Ala Ile Ser His Asp Ser Asp Pro Asn Ser
 340 345 350
 Ala Asn Thr Thr Thr Ile Glu Gly Ile Ala Asn Gln Arg Val Lys Glu
 355 360 365
 Cys Asn Arg Ile Leu Ala Met Ala Thr Glu Leu Ala Lys Phe Gly Val
 370 375 380
 Lys Thr Thr Glu Leu Pro Asp Gly Ile Gln Val His Gly Leu Asn Ser
 385 390 395 400
 Ile Lys Asp Leu Lys Val Pro Ser Asp Ser Ser Gly Pro Val Gly Val
 405 410 415
 Cys Thr Tyr Asp Asp His Arg Val Ala Met Ser Phe Ser Leu Leu Ala
 420 425 430

Gly Met Val Asn Ser Gln Asn Glu Arg Asp Glu Val Ala Asn Pro Val
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 Val Leu Ala Ala Leu Gly Ser Gly Thr Cys Arg Ile Lys Asn Leu Leu
 35 40 45
 His Ser Asp Asp Thr Glu Val Met Leu Asn Ala Leu Glu Arg Leu Gly
 50 55 60
 Ala Ala Thr Phe Ser Trp Glu Glu Gly Glu Val Leu Val Val Asn
 65 70 75 80
 Gly Lys Gly Gly Asn Leu Gln Ala Ser Ser Ser Pro Leu Tyr Leu Gly
 85 90 95
 Asn Ala Gly Thr Ala Ser Arg Phe Leu Thr Thr Val Ala Thr Leu Ala
 100 105 110
 Asn Ser Ser Thr Val Asp Ser Ser Val Leu Thr Gly Asn Asn Arg Met
 115 120 125
 Lys Gln Arg Pro Ile Gly Asp Leu Val Asp Ala Leu Thr Ala Asn Val
 130 135 140
 Leu Pro Leu Asn Thr Ser Lys Gly Arg Ala Ser Leu Pro Leu Lys Ile
 145 150 155 160
 Ala Ala Ser Gly Gly Phe Ala Gly Gly Asn Ile Asn Leu Ala Ala Lys
 165 170 175
 Val Ser Ser Gln Tyr Val Ser Ser Leu Leu Met Cys Ala Pro Tyr Ala
 180 185 190
 Lys Glu Pro Val Thr Leu Arg Leu Val Gly Gly Lys Pro Ile Ser Gln
 195 200 205
 Pro Tyr Ile Asp Met Thr Thr Ala Met Met Arg Ser Phe Gly Ile Asp
 210 215 220

Val Gln Lys Ser Thr Thr Glu Glu His Thr Tyr His Ile Pro Gln Gly
 225 230 235 240
 Arg Tyr Val Asn Pro Ala Glu Tyr Val Ile Glu Ser Asp Ala Ser Cys
 245 250 255
 Ala Thr Tyr Pro Leu Ala Val Ala Val Thr Gly Thr Thr Cys Thr
 260 265 270
 Val Pro Asn Ile Gly Ser Ala Ser Leu Gln Gly Asp Ala Arg Phe Ala
 275 280 285
 Val Glu Val Leu Arg Pro Met Gly Cys Thr Val Glu Gln Thr Glu Thr
 290 295 300
 Ser Thr Thr Val Thr Gly Pro Ser Asp Gly Ile Leu Arg Ala Thr Ser
 305 310 315 320
 Lys Arg Gly Tyr Gly Thr Asn Asp Arg Cys Val Pro Arg Cys Phe Arg
 325 330 335
 Thr Gly Ser His Arg Pro Met Glu Lys Ser Gln Thr Thr Pro Pro Val
 340 345 350
 Ser Ser Gly Ile Ala Asn Gln Arg Val Lys Glu Cys Asn Arg Ile Lys
 355 360 365
 Ala Met Lys Asp Glu Leu Ala Lys Phe Gly Val Ile Cys Arg Glu His
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 Asp Asp Gly Leu Glu Ile Asp Gly Ile Asp Arg Ser Asn Leu Arg Gln
 385 390 395 400
 Pro Val Gly Gly Val Phe Cys Tyr Asp Asp His Arg Val Ala Phe Ser
 405 410 415
 Phe Ser Val Leu Ser Leu Val Thr Pro Gln Pro Thr Leu Ile Leu Glu
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 Gln Leu Phe Lys Val Lys Leu Glu Gly Lys Glu Leu
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 <211> 444
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Asp	Asp	Ile	Asn	Tyr	Met	Leu	Asp	Ala	Leu	Lys	Lys	Leu	Gly	Leu	Asn
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Val	Glu	Arg	Asp	Ser	Val	Asn	Asn	Arg	Ala	Val	Val	Glu	Gly	Cys	Gly
65					70				75			80			
Gly	Ile	Phe	Pro	Ala	Ser	Leu	Asp	Ser	Lys	Ser	Asp	Ile	Glu	Leu	Tyr
					85			90				95			
Leu	Gly	Asn	Ala	Gly	Thr	Ala	Met	Arg	Pro	Leu	Thr	Ala	Ala	Val	Thr
					100			105			110				
Ala	Ala	Gly	Gly	Asn	Ala	Ser	Tyr	Val	Leu	Asp	Gly	Val	Pro	Arg	Met
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					165			170			175				
Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala
					180			185			190				
Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Ile	Asp	Lys	Leu	Ile	Ser	Val	Pro
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Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Val	Ser	Ala
					210			215			220				
Glu	His	Ser	Asp	Ser	Trp	Asp	Arg	Phe	Phe	Val	Lys	Gly	Gly	Gln	Lys
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Tyr	Lys	Ser	Pro	Gly	Asn	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala
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Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Ile	Thr	Gly	Glu	Thr	Val	Thr	Val
					260			265			270				
Glu	Gly	Cys	Gly	Thr	Thr	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu
					275			280			285				
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Thr	Val	Thr	Gly	Pro	Ser	Arg	Asp	Ala	Phe	Gly	Met	Arg	His	Leu	Arg
					305			310			315			320	

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 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
 340 345 350
 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
 355 360 365
 Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Ser Asp Tyr Cys
 370 375 380
 Val Ile Thr Pro Pro Ala Lys Val Lys Pro Ala Glu Ile Asp Thr Tyr
 385 390 395 400
 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
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 Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn Ser
 35 40 45
 Asp Asp Ile Asn Tyr Met Leu Asp Ala Leu Lys Arg Leu Gly Leu Asn
 50 55 60
 Val Glu Thr Asp Ser Glu Asn Asn Arg Ala Val Val Glu Gly Cys Gly
 65 70 75 80
 Gly Ile Phe Pro Ala Ser Ile Asp Ser Lys Ser Asp Ile Glu Leu Tyr
 85 90 95
 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
 100 105 110
 Ala Ala Gly Gly Asn Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met
 115 120 125
 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
 130 135 140

Ala Asp Val Glu Cys Thr Leu Gly Thr Asn Cys Pro Pro Val Arg Val
 145 150 155 160

 Asn Ala Asn Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
 165 170 175

 Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ser Ala Pro Leu Ala
 180 185 190

 Leu Gly Asp Val Glu Ile Glu Ile Val Asp Lys Leu Ile Ser Val Pro
 195 200 205

 Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Val
 210 215 220

 Glu His Ser Asp Ser Trp Asp Arg Phe Phe Val Lys Gly Gly Gln Lys
 225 230 235 240

 Tyr Lys Ser Pro Gly Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
 245 250 255

 Cys Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Glu Thr Val Thr Val
 260 265 270

 Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
 275 280 285

 Val Leu Glu Lys Met Gly Cys Lys Val Ser Trp Thr Glu Asn Ser Val
 290 295 300

 Thr Val Thr Gly Pro Pro Arg Asp Ala Phe Gly Met Arg His Leu Arg
 305 310 315 320

 Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
 325 330 335

 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
 340 345 350

 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
 355 360 365

 Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Ser Asp Tyr Cys
 370 375 380

 Val Ile Thr Pro Pro Lys Lys Val Lys Thr Ala Glu Ile Asp Thr Tyr
 385 390 395 400

 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
 405 410 415

 Val Pro Ile Thr Ile Asn Asp Ser Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430

 Asp Tyr Phe Gln Val Leu Glu Arg Ile Thr Lys His
 435 440

<210> 53
<211> 444
<212> PRT
<213> Nicotiana tabacum

<400> 53

Lys Pro Asn Glu Ile Val Leu Gln Pro Ile Lys Asp Ile Ser Gly Thr
1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Lys Gly Arg Thr Val Val Asp Asn Leu Leu Ser Ser
35 40 45

Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
50 55 60

Val Glu Asp Asp Asn Glu Asn Gln Arg Ala Ile Val Glu Gly Cys Gly
65 70 75 80

Gly Gln Phe Pro Val Gly Lys Ser Glu Glu Glu Ile Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Val Ala Gly Gly His Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
130 135 140

Ala Glu Val Asp Cys Phe Leu Gly Thr Asn Cys Pro Pro Val Arg Ile
145 150 155 160

Val Ser Lys Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Val
210 215 220

Glu His Thr Ser Ser Trp Asp Lys Phe Leu Val Arg Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Gly Lys Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Val Thr Gly Gly Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Ser Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Lys Gly Pro Pro Arg Asn Ser Ser Gly Met Lys His Leu Arg
305 310 315 320

Ala Val Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Val Glu Gly Ser Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Glu Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415

Val Pro Val Thr Ile Lys Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asn Tyr Phe Asp Val Leu Gln Gln Tyr Ser Lys His
435 440

<210> 54
<211> 444
<212> PRT
<213> Lycopersicon esculentum

<220>
<221> UNSURE
<222> (1)...(444)
<223> Xaa = any

<400> 54

Lys Pro His Glu Ile Val Leu Xaa Pro Ile Lys Asp Ile Ser Gly Thr
1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Glu Gly Arg Thr Val Val Asp Asn Leu Leu Ser Ser
35 40 45

Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
50 55 60

Val Glu Asp Asp Asn Glu Asn Gln Arg Ala Ile Val Glu Gly Cys Gly
 65 70 75 80
 Gly Gln Phe Pro Val Gly Lys Lys Ser Glu Glu Glu Ile Gln Leu Phe
 85 90 95
 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
 100 105 110
 Val Ala Gly Gly His Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
 115 120 125
 Arg Glu Arg Pro Ile Gly Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
 130 135 140
 Ala Glu Val Asp Cys Ser Leu Gly Thr Asn Cys Pro Pro Val Arg Ile
 145 150 155 160
 Val Ser Lys Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
 165 170 175
 Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
 180 185 190
 Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
 195 200 205
 Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Phe Val
 210 215 220
 Glu His Ser Ser Gly Trp Asp Arg Phe Leu Val Lys Gly Gly Gln Lys
 225 230 235 240
 Tyr Lys Ser Pro Gly Lys Ala Phe Val Glu Gly Asp Ala Ser Ser Ala
 245 250 255
 Ser Tyr Phe Leu Ala Gly Ala Ala Val Thr Gly Gly Thr Val Thr Val
 260 265 270
 Glu Gly Cys Gly Thr Ser Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
 275 280 285
 Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
 290 295 300
 Thr Val Lys Gly Pro Pro Arg Asn Ser Ser Gly Met Lys His Leu Arg
 305 310 315 320
 Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
 325 330 335
 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
 340 345 350
 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
 355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Val Glu Gly Ser Asp Tyr Cys
 370 375 380
 Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Glu Ile Asp Thr Tyr
 385 390 395 400
 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
 405 410 415
 Val Pro Val Thr Ile Lys Asn Pro Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430
 Asp Tyr Phe Glu Val Leu Gln Lys Tyr Ser Lys His
 435 440
 <210> 55
 <211> 444
 <212> PRT
 <213> Petunia x hybrida
 <400> 55
 Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly Thr
 1 5 10 15
 Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
 20 25 30
 Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Ser Ser
 35 40 45
 Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
 50 55 60
 Val Glu Glu Asp Ser Ala Asn Gln Arg Ala Val Val Glu Gly Cys Gly
 65 70 75 80
 Gly Leu Phe Pro Val Gly Lys Glu Ser Lys Glu Glu Ile Gln Leu Phe
 85 90 95
 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
 100 105 110
 Val Ala Gly Gly Asn Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
 115 120 125
 Arg Glu Arg Pro Ile Ser Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
 130 135 140
 Ala Glu Val Asp Cys Phe Leu Gly Thr Lys Cys Pro Pro Val Arg Ile
 145 150 155 160
 Val Ser Lys Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
 165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
 180 185 190
 Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
 195 200 205
 Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Ile Ser Val
 210 215 220
 Glu His Ser Ser Ser Trp Asp Arg Phe Phe Val Arg Gly Gly Gln Lys
 225 230 235 240
 Tyr Lys Ser Pro Gly Lys Ala Phe Val Glu Gly Asp Ala Ser Ser Ala
 245 250 255
 Ser Tyr Phe Leu Ala Gly Ala Ala Val Thr Gly Gly Thr Ile Thr Val
 260 265 270
 Glu Gly Cys Gly Thr Asn Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
 275 280 285
 Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
 290 295 300
 Thr Val Lys Gly Pro Pro Arg Ser Ser Ser Gly Arg Lys His Leu Arg
 305 310 315 320
 Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
 325 330 335
 Ala Val Val Ala Leu Tyr Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
 340 345 350
 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
 355 360 365
 Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Pro Asp Tyr Cys
 370 375 380
 Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Asp Ile Asp Thr Tyr
 385 390 395 400
 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
 405 410 415
 Val Pro Val Thr Ile Asn Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430
 Asn Tyr Phe Asp Val Leu Gln Gln Tyr Ser Lys His
 435 440
 <210> 56
 <211> 444
 <212> PRT
 <213> Zea mays
 <400> 56

Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
 1 5 10 15
 Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu
 20 25 30
 Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
 35 40 45
 Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
 50 55 60
 Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
 65 70 75 80
 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
 85 90 95
 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
 100 105 110
 Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
 115 120 125
 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
 130 135 140
 Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
 145 150 155 160
 Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
 165 170 175
 Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Pro
 180 185 190
 Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
 195 200 205
 Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
 210 215 220
 Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
 225 230 235 240
 Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
 245 250 255
 Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
 260 265 270
 Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
 275 280 285
 Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
 290 295 300

Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
 305 310 315 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
 325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
 340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
 355 360 365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
 370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
 385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
 405 410 415

Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430

Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
 435 440

<210> 57
 <211> 427
 <212> PRT
 <213> *Salmonella gallinarum*

<400> 57

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
 1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Ala
 20 25 30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
 35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
 50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
 65 70 75 80

Pro Leu Arg Ala Pro Gly Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly
 85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Gln Asn Glu
 100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
 115 120 125
 Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
 130 135 140
 Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
 145 150 155 160
 Asp Ile Glu Val Asp Gly Ser Val Ser Gln Phe Leu Thr Ala Leu
 165 170 175
 Leu Met Thr Ala Pro Leu Ala Pro Lys Asp Thr Ile Ile Arg Val Lys
 180 185 190
 Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
 195 200 205
 Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
 210 215 220
 Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
 225 230 235 240
 Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile Lys
 245 250 255
 Gly Gly Thr Val Lys Val Thr Gly Ile Gly Arg Lys Ser Met Gln Gly
 260 265 270
 Asp Ile Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Ile Thr
 275 280 285
 Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
 290 295 300
 Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
 305 310 315 320
 Thr Ala Leu Phe Ala Lys Gly Thr Thr Thr Leu Arg Asn Ile Tyr Asn
 325 330 335
 Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
 340 345 350
 Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
 355 360 365
 Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
 370 375 380
 His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400
 Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415

Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
 420 425

<210> 58
 <211> 427
 <212> PRT
 <213> *Salmonella typhimurium*

<400> 58

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
 1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Ala
 20 25 30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
 35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
 50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
 65 70 75 80

Pro Leu Arg Ala Ser Gly Thr Leu Glu Leu Phe Leu Gly Asn Ala Gly
 85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Gln Asn Glu
 100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
 115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
 130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
 145 150 155 160

Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
 165 170 175

Leu Met Thr Ala Pro Leu Ala Pro Glu Asp Thr Ile Ile Arg Val Lys
 180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
 195 200 205

Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
 210 215 220

Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
 225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Gly Ile Lys
 245 250 255

Gly Gly Thr Val Lys Val Thr Gly Ile Gly Gly Lys Ser Met Gln Gly
 260 265 270
 Asp Ile Arg Phe Ala Asp Val Leu His Lys Met Gly Ala Thr Ile Thr
 275 280 285
 Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
 290 295 300
 Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
 305 310 315 320
 Thr Ala Leu Phe Ala Lys Gly Thr Thr Leu Arg Asn Ile Tyr Asn
 325 330 335
 Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
 340 345 350
 Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
 355 360 365
 Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
 370 375 380
 His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400
 Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415
 Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
 420 425
 <210> 59
 <211> 427
 <212> PRT
 <213> Klebsiella pneumoniae
 <400> 59
 Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Thr Val
 1 5 10 15
 Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
 20 25 30
 Ala Leu Ala Arg Gly Thr Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
 35 40 45
 Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Val His Tyr
 50 55 60
 Val Leu Ser Ser Asp Arg Thr Arg Cys Glu Val Thr Gly Thr Gly Gly
 65 70 75 80

Pro	Leu	Gln	Ala	Gly	Ser	Ala	Leu	Glu	Leu	Phe	Leu	Gly	Asn	Ala	Gly
							85								95
Thr	Ala	Met	Arg	Pro	Leu	Ala	Ala	Leu	Cys	Leu	Gly	Ser	Asn	Asp	
							100							110	
Ile	Val	Leu	Thr	Gly	Glu	Pro	Arg	Met	Lys	Glu	Arg	Pro	Ile	Gly	His
							115							125	
Leu	Val	Asp	Ala	Leu	Arg	Gln	Gly	Gly	Ala	Gln	Ile	Asp	Tyr	Leu	Glu
							130							140	
Gln	Glu	Asn	Tyr	Pro	Pro	Leu	Arg	Leu	Arg	Gly	Gly	Phe	Thr	Gly	Gly
							145							155	
Asp	Val	Glu	Val	Asp	Gly	Ser	Val	Ser	Ser	Gln	Phe	Leu	Thr	Ala	Leu
							165							175	
Leu	Met	Ala	Ser	Pro	Leu	Ala	Pro	Gln	Asp	Thr	Val	Ile	Ala	Ile	Lys
							180							190	
Gly	Glu	Leu	Val	Ser	Arg	Pro	Tyr	Ile	Asp	Ile	Thr	Leu	His	Leu	Met
							195							205	
Lys	Thr	Phe	Gly	Val	Glu	Val	Glu	Asn	Gln	Ala	Tyr	Gln	Arg	Phe	Ile
							210							220	
Val	Arg	Gly	Asn	Gln	Gln	Tyr	Gln	Ser	Pro	Gly	Asp	Tyr	Leu	Val	Glu
							225							240	
Gly	Asp	Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala	Ala	Gly	Ala	Ile	Lys
							245							255	
Gly	Gly	Thr	Val	Lys	Val	Thr	Gly	Ile	Gly	Arg	Asn	Ser	Val	Gln	Gly
							260							270	
Asp	Ile	Arg	Phe	Ala	Asp	Val	Leu	Glu	Lys	Met	Gly	Ala	Thr	Val	Thr
							275							285	
Trp	Gly	Glu	Asp	Tyr	Ile	Ala	Cys	Thr	Arg	Gly	Glu	Leu	Asn	Ala	Ile
							290							300	
Asp	Met	Asp	Met	Asn	His	Ile	Pro	Asp	Ala	Ala	Met	Thr	Ile	Ala	Thr
							305							320	
Ala	Ala	Leu	Phe	Ala	Arg	Gly	Thr	Thr	Leu	Arg	Asn	Ile	Tyr	Asn	
							325							335	
Trp	Arg	Val	Lys	Glu	Thr	Asp	Arg	Leu	Phe	Ala	Met	Ala	Thr	Glu	Leu
							340							350	
Arg	Lys	Val	Gly	Ala	Glu	Val	Glu	Glu	Gly	Glu	Asp	Tyr	Ile	Arg	Ile
							355							365	
Thr	Pro	Pro	Leu	Thr	Leu	Gln	Phe	Ala	Glu	Ile	Gly	Thr	Tyr	Asn	Asp
							370							380	

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400
 Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415
 Phe Gly Gln Leu Ala Arg Ile Ser Thr Leu Ala
 420 425
 <210> 60
 <211> 427
 <212> PRT
 <213> Yersinia enterocolitica
 <400> 60
 Met Leu Glu Ser Leu Thr Leu His Pro Ile Ala Leu Ile Asn Gly Thr
 1 5 10 15
 Val Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu
 20 25 30
 Ala Ala Leu Ala Glu Gly Thr Thr Gln Leu Asn Asn Leu Leu Asp Ser
 35 40 45
 Asp Asp Ile Arg His Met Leu Asn Ala Leu Gln Ala Leu Gly Val Lys
 50 55 60
 Tyr Arg Leu Ser Ala Asp Arg Thr Arg Cys Glu Val Asp Gly Leu Gly
 65 70 75 80
 Gly Lys Leu Val Ala Glu Gln Pro Leu Glu Leu Phe Leu Gly Asn Ala
 85 90 95
 Gly Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Lys Asn
 100 105 110
 Asp Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly
 115 120 125
 His Leu Val Asp Ala Leu Arg Gln Gly Gly Ala Gln Ile Asp Tyr Leu
 130 135 140
 Glu Gln Glu Asn Tyr Arg Arg Cys Ile Ala Gly Gly Phe Arg Gly Gly
 145 150 155 160
 Lys Leu Thr Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
 165 170 175
 Leu Met Thr Ala Pro Leu Ala Glu Gln Asp Thr Glu Ile Gln Ile Gln
 180 185 190
 Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu His Leu Met
 195 200 205
 Lys Ala Phe Gly Val Asp Val Val His Glu Asn Tyr Gln Ile Phe His
 210 215 220

Ile Lys Gly Gly Gln Thr Tyr Arg Ser Pro Gly Ile Tyr Leu Val Glu
 225 230 235 240
 Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Ala Ala Ile Lys
 245 250 255
 Gly Gly Thr Val Arg Val Thr Gly Ile Gly Lys Gln Ser Val Gln Gly
 260 265 270
 Asp Thr Lys Phe Ala Asp Val Leu Glu Lys Met Gly Ala Lys Ile Ser
 275 280 285
 Trp Gly Asp Asp Tyr Ile Glu Cys Ser Arg Gly Glu Leu Gln Gly Ile
 290 295 300
 Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
 305 310 315 320
 Thr Ala Leu Phe Ala Asp Gly Pro Thr Val Ile Arg Asn Ile Tyr Asn
 325 330 335
 Trp Arg Val Lys Glu Thr Asp Arg Leu Ser Ala Met Ala Thr Glu Leu
 340 345 350
 Arg Lys Val Gly Ala Glu Val Glu Glu Gly Gln Asp Tyr Ile Arg Val
 355 360 365
 Val Pro Pro Ala Gln Leu Ile Ala Ala Glu Ile Gly Thr Tyr Asn Asp
 370 375 380
 His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400
 Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415
 Phe Glu Gln Leu Ala Arg Leu Ser Gln Ile Ala
 420 425
 <210> 61
 <211> 432
 <212> PRT
 <213> Haemophilus influenzae
 <400> 61
 Met Glu Lys Ile Thr Leu Ala Pro Ile Ser Ala Val Glu Gly Thr Ile
 1 5 10 15
 Asn Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ala Leu Leu Leu Ala
 20 25 30
 Ala Leu Ala Lys Gly Thr Thr Lys Val Thr Asn Leu Leu Asp Ser Asp
 35 40 45

Asp Ile Arg His Met Leu Asn Ala Leu Lys Ala Leu Gly Val Arg Tyr
 50 55 60

Gln Leu Ser Asp Asp Lys Thr Ile Cys Glu Ile Glu Gly Leu Gly Gly
 65 70 75 80

Ala Phe Asn Ile Gln Asp Asn Leu Ser Leu Phe Leu Gly Asn Ala Gly
 85 90 95

Thr Ala Met Arg Pro Leu Thr Ala Ala Leu Cys Leu Lys Gly Asn His
 100 105 110

Glu Val Glu Ile Ile Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro
 115 120 125

Ile Leu His Leu Val Asp Ala Leu Arg Gln Ala Gly Ala Asp Ile Arg
 130 135 140

Tyr Leu Glu Asn Glu Gly Tyr Pro Pro Leu Ala Ile Arg Asn Lys Gly
 145 150 155 160

Ile Lys Gly Gly Lys Val Lys Ile Asp Gly Ser Ile Ser Ser Gln Phe
 165 170 175

Leu Thr Ala Leu Leu Met Ser Ala Pro Leu Ala Glu Asn Asp Thr Glu
 180 185 190

Ile Glu Ile Ile Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr
 195 200 205

Leu Ala Met Met Arg Asp Phe Gly Val Lys Val Glu Asn His His Tyr
 210 215 220

Gln Lys Phe Gln Val Lys Gly Asn Gln Ser Tyr Ile Ser Pro Asn Lys
 225 230 235 240

Tyr Leu Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala
 245 250 255

Gly Ala Ile Lys Gly Lys Val Lys Val Thr Gly Ile Gly Lys Asn Ser
 260 265 270

Ile Gln Gly Asp Arg Leu Phe Ala Asp Val Leu Glu Lys Met Gly Ala
 275 280 285

Lys Ile Thr Trp Gly Glu Asp Phe Ile Gln Ala Glu His Ala Glu Leu
 290 295 300

Asn Gly Ile Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr
 305 310 315 320

Ile Ala Thr Thr Ala Leu Phe Ser Asn Gly Glu Thr Val Ile Arg Asn
 325 330 335

Ile Tyr Asn Trp Arg Val Lys Glu Thr Asp Arg Leu Thr Ala Met Ala
 340 345 350

Thr Glu Leu Arg Lys Val Gly Ala Glu Val Glu Glu Gly Glu Asp Phe
 355 360 365
 Ile Arg Ile Gln Pro Leu Ala Leu Asn Gln Phe Lys His Ala Asn Ile
 370 375 380
 Glu Thr Tyr Asn Asp His Arg Met Ala Met Cys Phe Ser Leu Ile Ala
 385 390 395 400
 Leu Ser Asn Thr Pro Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys
 405 410 415
 Thr Phe Pro Thr Phe Phe Asn Glu Phe Glu Lys Ile Cys Leu Lys Asn
 420 425 430
 <210> 62
 <211> 441
 <212> PRT
 <213> *Pasteurella multocida*
 <400> 62
 Val Ile Lys Asp Ala Thr Ala Ile Thr Leu Asn Pro Ile Ser Tyr Ile
 1 5 10 15
 Glu Gly Glu Val Arg Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ala
 20 25 30
 Leu Leu Leu Ser Ala Leu Ala Lys Gly Lys Thr Thr Leu Thr Asn Leu
 35 40 45
 Leu Asp Ser Asp Asp Val Arg His Met Leu Asn Ala Leu Lys Glu Leu
 50 55 60
 Gly Val Thr Tyr Gln Leu Ser Glu Asp Lys Ser Val Cys Glu Ile Glu
 65 70 75 80
 Gly Leu Gly Arg Ala Phe Glu Trp Gln Ser Gly Leu Ala Leu Phe Leu
 85 90 95
 Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Leu Cys Leu
 100 105 110
 Ser Thr Pro Asn Arg Glu Gly Lys Asn Glu Ile Val Leu Thr Gly Glu
 115 120 125
 Pro Arg Met Lys Glu Arg Pro Ile Gln His Leu Val Asp Ala Leu Cys
 130 135 140
 Gln Ala Gly Ala Glu Ile Gln Tyr Leu Glu Gln Glu Gly Tyr Pro Pro
 145 150 155 160
 Ile Ala Ile Arg Asn Thr Gly Leu Lys Gly Gly Arg Ile Gln Ile Asp
 165 170 175
 Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu Leu Met Ala Ala Pro
 180 185 190

Met Ala Glu Ala Asp Thr Glu Ile Glu Ile Ile Gly Glu Leu Val Ser
 195 200 205
 Lys Pro Tyr Ile Asp Ile Thr Leu Lys Met Met Gln Thr Phe Gly Val
 210 215 220
 Glu Val Glu Asn Gln Ala Tyr Gln Arg Phe Leu Val Lys Gly His Gln
 225 230 235 240
 Gln Tyr Gln Ser Pro His Arg Phe Leu Val Glu Gly Asp Ala Ser Ser
 245 250 255
 Ala Ser Tyr Phe Leu Ala Ala Ala Ile Lys Gly Lys Val Lys Val
 260 265 270
 Thr Gly Val Gly Lys Asn Ser Ile Gln Gly Asp Arg Leu Phe Ala Asp
 275 280 285
 Val Leu Glu Lys Met Gly Ala His Ile Thr Trp Gly Asp Asp Phe Ile
 290 295 300
 Gln Val Glu Lys Gly Asn Leu Lys Gly Ile Asp Met Asp Met Asn His
 305 310 315 320
 Ile Pro Asp Ala Ala Met Thr Ile Ala Thr Thr Ala Leu Phe Ala Glu
 325 330 335
 Gly Glu Thr Val Ile Arg Asn Ile Tyr Asn Trp Arg Val Lys Glu Thr
 340 345 350
 Asp Arg Leu Thr Ala Met Ala Thr Glu Leu Arg Lys Val Gly Ala Glu
 355 360 365
 Val Glu Glu Gly Glu Asp Phe Ile Arg Ile Gln Pro Leu Asn Leu Ala
 370 375 380
 Gln Phe Gln His Ala Glu Leu Asn Ile His Asp His Arg Met Ala Met
 385 390 395 400
 Cys Phe Ala Leu Ile Ala Leu Ser Lys Thr Ser Val Thr Ile Leu Asp
 405 410 415
 Pro Ser Cys Thr Ala Lys Thr Phe Pro Thr Phe Leu Ile Leu Phe Thr
 420 425 430
 Leu Asn Thr Arg Glu Val Ala Tyr Arg
 435 440

<210> 63
<211> 426
<212> PRT
<213> Aeromonas salmonicida

<400> 63

Asn Ser Leu Arg Leu Glu Pro Ile Ser Arg Val Ala Gly Glu Val Asn
1 5 10 15

Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Ala Ala
20 25 30

Leu Ala Arg Gly Thr Thr Arg Leu Thr Asn Leu Leu Asp Ser Asp Asp
35 40 45

Ile Arg His Met Leu Ala Ala Leu Thr Gln Leu Gly Val Lys Tyr Lys
50 55 60

Leu Ser Ala Asp Lys Thr Glu Cys Thr Val His Gly Leu Gly Arg Ser
65 70 75 80

Phe Ala Val Ser Ala Pro Val Asn Leu Phe Leu Gly Asn Ala Gly Thr
85 90 95

Ala Met Arg Pro Leu Cys Ala Ala Leu Cys Leu Gly Ser Gly Glu Tyr
100 105 110

Met Leu Gly Gly Glu Pro Arg Met Glu Glu Arg Pro Ile Gly His Leu
115 120 125

Val Asp Cys Leu Ala Leu Lys Gly Ala His Ile Gln Tyr Leu Lys Lys
130 135 140

Asp Gly Tyr Pro Pro Leu Val Val Asp Ala Lys Gly Leu Trp Gly Gly
145 150 155 160

Asp Val His Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Phe
165 170 175

Leu Met Ala Ala Pro Ala Met Ala Pro Val Ile Pro Arg Ile His Ile
180 185 190

Lys Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu His Ile
195 200 205

Met Asn Ser Ser Gly Val Val Ile Glu His Asp Asn Tyr Lys Leu Phe
210 215 220

Tyr Ile Lys Gly Asn Gln Ser Ile Val Ser Pro Gly Asp Phe Leu Val
225 230 235 240

Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile
245 250 255

Lys Gly Lys Val Arg Val Thr Gly Ile Gly Lys His Ser Ile Gly Asp
260 265 270

Ile His Phe Ala Asp Val Leu Glu Arg Met Gly Ala Arg Ile Thr Trp
 275 280 285
 Gly Asp Asp Phe Ile Glu Ala Glu Gln Gly Pro Leu His Gly Val Asp
 290 295 300
 Met Asp Met Asn His Ile Pro Asp Val Gly His Asp His Ser Gly Gln
 305 310 315 320
 Ser His Cys Leu Pro Arg Val Pro Pro His Ser Gln His Leu Gln Leu
 325 330 335
 Ala Val Arg Asp Asp Arg Cys Thr Pro Cys Thr His Gly His Arg Arg
 340 345 350
 Ala Gln Ala Gly Val Ser Glu Glu Gly Thr Thr Phe Ile Thr Arg Asp
 355 360 365
 Ala Ala Asp Pro Ala Gln Ala Arg Arg Asp Arg His Leu Gln Arg Ser
 370 375 380
 Arg Ile Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Ile Ala Val
 385 390 395 400
 Thr Ile Asn Asp Pro Gly Cys Thr Ser Lys Thr Phe Pro Asp Tyr Phe
 405 410 415
 Asp Lys Leu Ala Ser Val Ser Gln Ala Val
 420 425
 <210> 64
 <211> 442
 <212> PRT
 <213> *Bacillus pertussis*
 <400> 64
 Met Ser Gly Leu Ala Tyr Leu Asp Leu Pro Ala Ala Arg Leu Ala Arg
 1 5 10 15
 Gly Glu Val Ala Leu Pro Gly Ser Lys Ser Ile Ser Asn Arg Val Leu
 20 25 30
 Leu Leu Ala Ala Leu Ala Glu Gly Ser Thr Glu Ile Thr Gly Leu Leu
 35 40 45
 Asp Ser Asp Asp Thr Arg Val Met Leu Ala Ala Leu Arg Gln Leu Gly
 50 55 60
 Val Ser Val Gly Glu Val Ala Asp Gly Cys Val Thr Ile Glu Gly Val
 65 70 75 80
 Ala Arg Phe Pro Thr Glu Gln Ala Glu Leu Phe Leu Gly Asn Ala Gly
 85 90 95

Thr Ala Phe Arg Pro Leu Thr Ala Ala Leu Ala Leu Met Gly Gly Asp
 100 105 110
 Tyr Arg Leu Ser Gly Val Pro Arg Met His Glu Arg Pro Ile Gly Asp
 115 120 125
 Leu Val Asp Ala Leu Arg Gln Phe Gly Ala Gly Ile Glu Tyr Leu Gly
 130 135 140
 Gln Ala Gly Tyr Pro Pro Leu Arg Ile Gly Gly Ser Ile Arg Val
 145 150 155 160
 Asp Gly Pro Val Arg Val Glu Gly Ser Val Ser Ser Gln Phe Leu Thr
 165 170 175
 Ala Leu Leu Met Ala Ala Pro Val Leu Ala Arg Arg Ser Gly Gln Asp
 180 185 190
 Ile Thr Ile Glu Val Val Gly Glu Leu Ile Ser Lys Pro Tyr Ile Glu
 195 200 205
 Ile Thr Leu Asn Leu Met Ala Arg Phe Gly Val Ser Val Arg Arg Asp
 210 215 220
 Gly Trp Arg Ala Phe Thr Ile Ala Arg Asp Ala Val Tyr Arg Gly Pro
 225 230 235 240
 Gly Arg Met Ala Ile Glu Gly Asp Ala Ser Thr Ala Ser Tyr Phe Leu
 245 250 255
 Ala Leu Gly Ala Ile Gly Gly Pro Val Arg Val Thr Gly Val Gly
 260 265 270
 Glu Asp Ser Ile Gln Gly Asp Val Ala Phe Ala Ala Thr Leu Ala Ala
 275 280 285
 Met Gly Ala Asp Val Arg Tyr Gly Pro Gly Trp Ile Glu Thr Arg Gly
 290 295 300
 Val Arg Val Ala Glu Gly Gly Arg Leu Lys Ala Phe Asp Ala Asp Phe
 305 310 315 320
 Asn Leu Ile Pro Asp Ala Ala Met Thr Ala Ala Thr Leu Ala Leu Tyr
 325 330 335
 Ala Asp Gly Pro Cys Arg Leu Arg Asn Ile Gly Ser Trp Arg Val Lys
 340 345 350
 Glu Thr Asp Arg Ile His Ala Met His Thr Glu Leu Glu Lys Leu Gly
 355 360 365
 Ala Gly Val Gln Ser Gly Ala Asp Trp Leu Glu Val Ala Pro Pro Glu
 370 375 380
 Pro Gly Gly Trp Arg Asp Ala His Ile Gly Thr Trp Asp Asp His Arg
 385 390 395 400

Met Ala Met Cys Phe Leu Leu Ala Ala Phe Gly Pro Ala Ala Val Arg
 405 410 415
 Ile Leu Asp Pro Gly Cys Val Ser Lys Thr Phe Pro Asp Tyr Phe Asp
 420 425 430
 Val Tyr Ala Gly Leu Leu Ala Ala Arg Asp
 435 440
 <210> 65
 <211> 427
 <212> PRT
 <213> *Salmonella typhimurium*
 <400> 65
 Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
 1 5 10 15
 Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Ala
 20 25 30
 Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
 35 40 45
 Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
 50 55 60
 Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
 65 70 75 80
 Pro Leu Arg Ala Ser Gly Thr Leu Glu Leu Phe Leu Gly Asn Ala Gly
 85 90 95
 Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Gln Asn Glu
 100 105 110
 Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
 115 120 125
 Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
 130 135 140
 Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
 145 150 155 160
 Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
 165 170 175
 Leu Met Thr Ala Pro Leu Ala Pro Glu Asp Thr Ile Ile Arg Val Lys
 180 185 190
 Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
 195 200 205
 Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
 210 215 220

Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Gly Ile Lys
245 250 255

Gly Gly Thr Val Lys Val Thr Gly Ile Gly Gly Lys Ser Met Gln Gly
260 265 270

Asp Ile Arg Phe Ala Asp Val Leu His Lys Met Gly Ala Thr Ile Thr
275 280 285

Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
290 295 300

Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
305 310 315 320

Thr Ala Leu Phe Ala Lys Gly Thr Thr Leu Arg Asn Ile Tyr Asn
325 330 335

Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
340 345 350

Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
355 360 365

Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
370 375 380

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
385 390 395 400

Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
405 410 415

Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
420 425

<210> 66
<211> 1894
<212> DNA
<213> Synechocystis sp.

<220>
<221> CDS
<222> (275)..(1618)

<400> 66
acgggctgta acggtagtag gggtccc gag cacaaggcg gtgccggcaa gcagaactaa 60
tttccatggg gaataatggt attcattgg tttggcctct ggtctggcaa tggttgctag 120
gcgatcgctt gttgaaattha acaaactgtc gcccttccac tgaccatggt aacgatgttt 180
tttacttcct tgactaaccg aggaaaattt ggcggggggc agaaatgcca atacaattta 240

gcttggtctt ccctgcccct aatttgcctt ctcc atg gcc ttg ctt tcc ctc aac Met Ala Leu Leu Ser Leu Asn 1 5	295
aat cat caa tcc cat caa cgc tta act gtt aat ccc cct gcc caa ggg Asn His Gln Ser His Gln Arg Leu Thr Val Asn Pro Pro Ala Gln Gly 10 15 20	343
gtc gct ttg act ggc cgc cta agg gtg ccg ggg gat aaa tcc att tcc Val Ala Leu Thr Gly Arg Leu Arg Val Pro Gly Asp Lys Ser Ile Ser 25 30 35	391
cat cgg gcc ttg atg ttg ggg gcg atc gcc acc ggg gaa acc att atc His Arg Ala Leu Met Leu Gly Ala Ile Ala Thr Gly Glu Thr Ile Ile 40 45 50 55	439
gaa ggg cta ctg ttg ggg gaa gat ccc cgt agt acg gcc cat tgc ttt Glu Gly Leu Leu Gly Glu Asp Pro Arg Ser Thr Ala His Cys Phe 60 65 70	487
cgg gcc atg gga gca gaa atc agc gaa cta aat tca gaa aaa atc atc Arg Ala Met Gly Ala Glu Ile Ser Glu Leu Asn Ser Glu Lys Ile Ile 75 80 85	535
gtt cag ggt cgg ggt ctg gga cag ttg cag gaa ccc agt acc gtt ttg Val Gln Gly Arg Gly Leu Gly Gln Leu Gln Glu Pro Ser Thr Val Leu 90 95 100	583
gat gcg ggg aac tct ggc acc acc atg cgc tta atg ttg ggc ttg cta Asp Ala Gly Asn Ser Gly Thr Thr Met Arg Leu Met Leu Gly Leu Leu 105 110 115	631
gcc ggg caa aaa gat tgt tta ttc acc gtc acc ggc gat gat tcc ctc Ala Gly Gln Lys Asp Cys Leu Phe Thr Val Thr Gly Asp Asp Ser Leu 120 125 130 135	679
cgt cac cgc ccc atg tcc cgg gta att caa ccc ttg caa caa atg ggg Arg His Arg Pro Met Ser Arg Val Ile Gln Pro Leu Gln Gln Met Gly 140 145 150	727
gca aaa att tgg gcc cgg agt aac ggc aag ttt gcg ccg ctg gca gtc Ala Lys Ile Trp Ala Arg Ser Asn Gly Lys Phe Ala Pro Leu Ala Val 155 160 165	775
cag ggt agc caa tta aaa ccg atc cat tac cat tcc ccc att gct tca Gln Gly Ser Gln Leu Lys Pro Ile His Tyr His Ser Pro Ile Ala Ser 170 175 180	823
gcc cag gta aag tcc tgc ctg ttg cta gcg ggg tta acc acc gag ggg Ala Gln Val Lys Ser Cys Leu Leu Leu Ala Gly Leu Thr Thr Glu Gly 185 190 195	871
gac acc acg gtt aca gaa cca gct cta tcc cgg gat cat agc gaa cgc Asp Thr Thr Val Thr Glu Pro Ala Leu Ser Arg Asp His Ser Glu Arg 200 205 210 215	919

atg ttg cag gcc ttt gga gcc aaa tta acc att gat cca gta acc cat Met Leu Gln Ala Phe Gly Ala Lys Leu Thr Ile Asp Pro Val Thr His 220 225 230	967
agc gtc act gtc cat ggc ccg gcc cat tta acg ggg caa cgg gtg gtg Ser Val Thr Val His Gly Pro Ala His Leu Thr Gly Gln Arg Val Val 235 240 245	1015
gtg cca ggg gac atc agc tcg gcg gcc ttt tgg tta gtg gcg gca tcc Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu Val Ala Ala Ser 250 255 260	1063
att ttg cct gga tca gaa ttg ttg gtg gaa aat gta ggc att aac ccc Ile Leu Pro Gly Ser Glu Leu Leu Val Glu Asn Val Gly Ile Asn Pro 265 270 275	1111
acc agg aca ggg gtg ttg gaa gtg ttg gcc cag atg ggg gcg gac att Thr Arg Thr Gly Val Leu Glu Val Leu Ala Gln Met Gly Ala Asp Ile 280 285 290 295	1159
acc ccg gag aat gaa cga ttg gta acg ggg gaa ccg gta gca gat ctg Thr Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp Leu 300 305 310	1207
cggtt agg gca agc cat ctc cag ggt tgc acc ttc ggc ggc gaa att Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu Ile 315 320 325	1255
att ccc cga ctg att gat gaa att ccc att ttg gca gtg gcg gcg gcc Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala Ala 330 335 340	1303
ttt gca gag ggc act acc cgc att gaa gat gcc gca gaa ctg agg gtt Phe Ala Glu Gly Thr Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg Val 345 350 355	1351
aaa gaa agc gat cgc ctg gcg gcc att gct tcg gag ttg ggc aaa atg Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys Met 360 365 370 375	1399
ggg gcc aaa gtc acc gaa ttt gat gat ggc ctg gaa att caa ggg gga Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly Gly 380 385 390	1447
agc ccg tta caa ggg gcc gag gtg gat agc ttg acg gat cat cgc att Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Leu Thr Asp His Arg Ile 395 400 405	1495
gcc atg gcg ttg gcg atc gcc gct tta ggt agt ggg ggg caa aca att Ala Met Ala Leu Ala Ile Ala Ala Leu Gly Ser Gly Gly Gln Thr Ile 410 415 420	1543
att aac cgg gcg gaa gcg gcc gcc att tcc tat cca gaa ttt ttt ggc Ile Asn Arg Ala Glu Ala Ala Ala Ser Tyr Pro Glu Phe Phe Gly 425 430 435	1591

acg cta ggg caa gtt gcc caa gga taa agtttagaaaa	actcctggc	1638	
Thr Leu Gly Gln Val Ala Gln Gly			
440	445		
ggtttgtaaa tgttttacca aggttagtttgc gggtaaaggc cccagcaagt gctgccaggg		1698	
taatttatcc gcaattgacc aatcggcatg gaccgtatcg ttcaaaactgg gtaattctcc		1758	
ctttaattcc ttaaaagctc gcttaaaact gcccaacgta tctccgtaat ggcgagttag		1818	
tagaagtaat ggggccaaac ggcgatcgcc acggaaatt aaagcctgca tcactgacca		1878	
cttataactt tcggga		1894	
<210> 67			
<211> 447			
<212> PRT			
<213> Synechocystis sp.			
<400> 67			
Met Ala Leu Leu Ser Leu Asn Asn His Gln Ser His Gln Arg Leu Thr			
1	5	10	15
Val Asn Pro Pro Ala Gln Gly Val Ala Leu Thr Gly Arg Leu Arg Val			
20	25	30	
Pro Gly Asp Lys Ser Ile Ser His Arg Ala Leu Met Leu Gly Ala Ile			
35	40	45	
Ala Thr Gly Glu Thr Ile Ile Glu Gly Leu Leu Leu Gly Glu Asp Pro			
50	55	60	
Arg Ser Thr Ala His Cys Phe Arg Ala Met Gly Ala Glu Ile Ser Glu			
65	70	75	80
Leu Asn Ser Glu Lys Ile Ile Val Gln Gly Arg Gly Leu Gly Gln Leu			
85	90	95	
Gln Glu Pro Ser Thr Val Leu Asp Ala Gly Asn Ser Gly Thr Thr Met			
100	105	110	
Arg Leu Met Leu Gly Leu Leu Ala Gly Gln Lys Asp Cys Leu Phe Thr			
115	120	125	
Val Thr Gly Asp Asp Ser Leu Arg His Arg Pro Met Ser Arg Val Ile			
130	135	140	
Gln Pro Leu Gln Gln Met Gly Ala Lys Ile Trp Ala Arg Ser Asn Gly			
145	150	155	160
Lys Phe Ala Pro Leu Ala Val Gln Gly Ser Gln Leu Lys Pro Ile His			
165	170	175	
Tyr His Ser Pro Ile Ala Ser Ala Gln Val Lys Ser Cys Leu Leu Leu			
180	185	190	

Ala Gly Leu Thr Thr Glu Gly Asp Thr Thr Val Thr Glu Pro Ala Leu
 195 200 205
 Ser Arg Asp His Ser Glu Arg Met Leu Gln Ala Phe Gly Ala Lys Leu
 210 215 220
 Thr Ile Asp Pro Val Thr His Ser Val Thr Val His Gly Pro Ala His
 225 230 235 240
 Leu Thr Gly Gln Arg Val Val Val Pro Gly Asp Ile Ser Ser Ala Ala
 245 250 255
 Phe Trp Leu Val Ala Ala Ser Ile Leu Pro Gly Ser Glu Leu Leu Val
 260 265 270
 Glu Asn Val Gly Ile Asn Pro Thr Arg Thr Gly Val Leu Glu Val Leu
 275 280 285
 Ala Gln Met Gly Ala Asp Ile Thr Pro Glu Asn Glu Arg Leu Val Thr
 290 295 300
 Gly Glu Pro Val Ala Asp Leu Arg Val Arg Ala Ser His Leu Gln Gly
 305 310 315 320
 Cys Thr Phe Gly Gly Glu Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro
 325 330 335
 Ile Leu Ala Val Ala Ala Phe Ala Glu Gly Thr Thr Arg Ile Glu
 340 345 350
 Asp Ala Ala Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Ile
 355 360 365
 Ala Ser Glu Leu Gly Lys Met Gly Ala Lys Val Thr Glu Phe Asp Asp
 370 375 380
 Gly Leu Glu Ile Gln Gly Gly Ser Pro Leu Gln Gly Ala Glu Val Asp
 385 390 395 400
 Ser Leu Thr Asp His Arg Ile Ala Met Ala Leu Ala Ile Ala Ala Leu
 405 410 415
 Gly Ser Gly Gly Gln Thr Ile Ile Asn Arg Ala Glu Ala Ala Ile
 420 425 430
 Ser Tyr Pro Glu Phe Phe Gly Thr Leu Gly Gln Val Ala Gln Gly
 435 440 445

<210> 68
 <211> 1479
 <212> DNA
 <213> *Dichelobacter nodosus*

<220>
 <221> CDS
 <222> (107)..(1438)

<400> 68 tttaaaaaaca atgagttaaa aaattatttt tctggcacac gcgcttttt tgcattttt ctccccatttt tccggcacaa taacgttggt tttataaaag gaaatg atg atg acg aat ata tgg cac acc gcg ccc gtc tct gcg ctt tcc ggc gaa ata acg Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr 5 10 15	60
 ata tgc ggc gat aaa tca atg tcg cat cgc gcc tta tta tta gca gcg Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Leu Ala Ala 20 25 30 35	115
 tta gca gaa gga caa acg gaa atc cgc ggc ttt tta gcg tgc gcg gat Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp 40 45 50	163
 tgt ttg gcg acg cgg caa gca ttg cgc gca tta ggc gtt gat att caa Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln 55 60 65	211
 aga gaa aaa gaa ata gtg acg att cgc ggt gtg gga ttt ctg ggt ttg Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu 70 75 80	259
 cag ccg ccg aaa gca ccg tta aat atg caa aac agt ggc act agc atg Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly Thr Ser Met 85 90 95	307
 cgt tta ttg gca gga att ttg gca gcg cag cgc ttt gag agc gtg tta Arg Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu 100 105 110 115	355
 tgc ggc gat gaa tca tta gaa aaa cgt ccg atg cag cgc att att acg Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr 120 125 130	403
 ccg ctt gtg caa atg ggg gca aaa att gtc agt cac agc aat ttt acg Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr 135 140 145	451
 gcg ccg tta cat att tca gga cgc ccg ctg acc ggc att gat tac gcg Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala 150 155 160	499
 tta ccg ctt ccc agc gcg caa tta aaa agt tgc ctt att ttg gca gga	547
	595
	643

Leu	Pro	Leu	Pro	Ser	Ala	Gln	Leu	Lys	Ser	Cys	Leu	Ile	Leu	Ala	Gly		
165																175	
tta	ttg	gct	gac	ggt	acc	acg	cg	ctg	cat	act	tgc	ggc	atc	agt	cgc	691	
Leu	Leu	Ala	Asp	Gly	Thr	Thr	Arg	Leu	His	Thr	Cys	Gly	Ile	Ser	Arg		
180																195	
gac	cac	acg	gaa	cgc	atg	ttg	ccg	ctt	ttt	ggt	ggc	gca	ctt	gag	atc	739	
Asp	His	Thr	Glu	Arg	Met	Leu	Pro	Leu	Phe	Gly	Gly	Ala	Leu	Glu	Ile		
																200	
																205	
																210	
aag	aaa	gag	caa	ata	atc	gtc	acc	ggt	gga	caa	aaa	ttg	cac	ggt	tgc	787	
Lys	Lys	Glu	Gln	Ile	Ile	Val	Thr	Gly	Gly	Gln	Lys	Leu	His	Gly	Cys		
																215	
																220	
																225	
gtg	ctt	gat	att	gtc	ggc	gat	ttg	tcg	g	cg	g	cg	ttt	ttt	atg	gtt	835
Val	Leu	Asp	Ile	Val	Gly	Asp	Leu	Ser	Ala	Ala	Ala	Phe	Phe	Met	Val		
																230	
																235	
																240	
g	cg	g	ct	tt	g	att	g	cg	cc	g	aa	gt	tt	at	gt	883	
Ala	Ala	Leu	Ile	Ala	Pro	Arg	Ala	Glu	Val	Val	Ile	Arg	Asn	Val	Gly		
																245	
																250	
																255	
att	aat	ccg	acg	cg	gc	atc	att	act	ttg	ttg	caa	aaa	atg	gg		931	
Ile	Asn	Pro	Thr	Arg	Ala	Ala	Ile	Ile	Thr	Leu	Leu	Gln	Lys	Met	Gly		
																260	
																265	
																270	
																275	
g	ga	cg	att	gaa	ttg	cat	cat	cag	cg	ttt	tgg	gg	cc	g	tg	979	
Gly	Arg	Ile	Glu	Leu	His	His	Gln	Arg	Phe	Trp	Gly	Ala	Glu	Pro	Val		
																280	
																285	
																290	
g	ca	g	at	tt	gt	tt	cat	tca	aaa	ttg	cg	gc	att	ac	gt	gc	1027
Ala	Asp	Ile	Val	Val	Tyr	His	Ser	Lys	Leu	Arg	Gly	Ile	Thr	Val	Ala		
																295	
																300	
																305	
cc	g	aa	tgg	att	gcc	aa	ac	gc	att	gat	gaa	ttg	cc	att	ttt	ttt	1075
Pro	Glu	Trp	Ile	Ala	Asn	Ala	Ile	Asp	Glu	Leu	Pro	Ile	Phe	Phe	Ile		
																310	
																315	
																320	
cg	g	ca	g	ct	gc	g	aa	gg	ac	ct	tt	gt	gg	aa	t	1123	
Ala	Ala	Ala	Cys	Ala	Glu	Gly	Thr	Thr	Phe	Val	Gly	Asn	Leu	Ser	Glu		
																325	
																330	
																335	
tt	g	cg	tt	gt	aa	gaa	tc	g	at	cg	g	cg	at	g	cg	1171	
Leu	Arg	Val	Lys	Glu	Ser	Asp	Arg	Leu	Ala	Ala	Met	Ala	Gln	Asn	Leu		
																340	
																345	
																350	
																355	
ca	aa	ct	tt	gg	gt	gc	g	ac	ct	tt	gt	gg	cc	at	tt	1219	
Gln	Thr	Leu	Gly	Val	Ala	Cys	Asp	Val	Gly	Ala	Asp	Phe	Ile	His	Ile		
																360	
																365	
																370	
ta	t	g	g	aa	g	at	cg	ca	tt	cc	g	cg	cg	cc	tt	1267	
Tyr	Gly	Arg	Ser	Asp	Arg	Gln	Phe	Leu	Pro	Ala	Arg	Val	Asn	Ser	Phe		
																375	
																380	
																385	
gg	cc	at	cg	tt	gg	at	g	cg	at	tt	gg	tt	gg	cc	cc	1315	
Gly	Asp	His	Arg	Ile	Ala	Met	Ser	Leu	Ala	Val	Ala	Gly	Val	Arg	Ala		

390	395	400	
gca ggt gaa tta ttg att gat gac ggc gcg gtg gcg gtc tct atg Ala Gly Leu Leu Ile Asp Asp Gly Ala Val Ala Ala Val Ser Met	405	410	1363
		415	
ccg caa ttt cgc gat ttt gcc gcc gca att ggt atg aat gta gga gaa Pro Gln Phe Arg Asp Phe Ala Ala Ile Gly Met Asn Val Gly Glu	420	425	1411
		430	
aaa gat gcg aaa aat tgt cac gat tga tggtcctagc ggtgttggaa Lys Asp Ala Lys Asn Cys His Asp	440		1458
aaggcacggt ggcgcaagct t			1479
<210> 69			
<211> 443			
<212> PRT			
<213> <i>Dichelobacter nodosus</i>			
<400> 69			
Met Met Thr Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly			
1	5	10	15
Glu Ile Thr Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu			
20	25		30
Leu Ala Ala Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala			
35	40		45
Cys Ala Asp Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val			
50	55	60	
Asp Ile Gln Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe			
65	70	75	80
Leu Gly Leu Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly			
85	90		95
Thr Ser Met Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu			
100	105		110
Ser Val Leu Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg			
115	120	125	
Ile Ile Thr Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser			
130	135	140	
Asn Phe Thr Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile			
145	150	155	160
Asp Tyr Ala Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile			
165	170	175	

Leu Ala Gly Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly
 180 185 190
 Ile Ser Arg Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala
 195 200 205
 Leu Glu Ile Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu
 210 215 220
 His Gly Cys Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe
 225 230 235 240
 Phe Met Val Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg
 245 250 255
 Asn Val Gly Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln
 260 265 270
 Lys Met Gly Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala
 275 280 285
 Glu Pro Val Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile
 290 295 300
 Thr Val Ala Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile
 305 310 315 320
 Phe Phe Ile Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn
 325 330 335
 Leu Ser Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala
 340 345 350
 Gln Asn Leu Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe
 355 360 365
 Ile His Ile Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val
 370 375 380
 Asn Ser Phe Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly
 385 390 395 400
 Val Arg Ala Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala
 405 410 415
 Val Ser Met Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn
 420 425 430
 Val Gly Glu Lys Asp Ala Lys Asn Cys His Asp
 435 440

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<210> 70
<211> 455
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 70

Met Leu His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
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Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
20 25 30

Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
35 40 45

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
50 55 60

Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
65 70 75 80

Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
85 90 95

Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
100 105 110

Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
115 120 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
130 135 140

Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
145 150 155 160

Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
180 185 190

Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205

Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
210 215 220

Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
225 230 235 240

Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
245 250 255

Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
260 265 270

Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
275 280 285

Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
290 295 300

Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
305 310 315 320

Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
325 330 335

Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
340 345 350

Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
355 360 365

Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
370 375 380

Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
385 390 395 400

His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
405 410 415

Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
420 425 430

Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
435 440 445

Leu Ser Asp Thr Lys Ala Ala
450 455

</U>